RECEIVED
MAR 11 2003
TECH CENTER 1600/2900

Please replace the paragraph beginning at page 8, line 1 with the following rewritten paragraph:

-- Figures 13A-F illustrate that the HSE-Tyr-300/HSF-1 feedback loop can be used to kill melanoma cells specifically and efficiently. Figures 13A and 13B show the effects of control (calcium phosphate only) transfections and transfection with CMV-GALV of non-melanoma TelCeB6 cells. Figures 13C-D show the effects of transfections of Me1624 cells with the HSE-Tyr-300 and Tyr-300-GALV constructs gave low levels of toxicity when transfected into a melanoma line, (or MeWo, not shown). Figures 13E-F show the effects of transfection with increasing amounts of co-transfected HSF-1d202-316 β-Gal plasmid.--

Please replace the paragraph beginning at page 14, line 8 with the following rewritten paragraph:

-- Methods of identifying promoter sequences are routine in the art. For example, in one embodiment of the invention, to identify a promoter sequence, the 5' portion of a gene is analyzed for the presence of sequences characteristic of promoter sequences, such as a TATA box consensus sequence (TATAAT), which is usually an AT-rich stretch of 5-10 base pair located approximately 20 to 40 base pair upstream of the transcription start site. In one embodiment, the location of a TATA box is determined using standard RNA-mapping techniques such as primer extension, S1 analysis, and/or RNase protection, to identify the position of the transcription start site within a genomic clone, and the TATA box is identified, either visually, or using a sequence search program. For example, sites important in transcriptional activation can be identified using the publicly available sequence search program TF SEARCH. Another publicly available database of sequences to which transcription factors bind is available from the National Library of Medicine in the "Transcription Data Base." --

Please replace the paragraph beginning at page 37, line 5 with the following rewritten paragraph:

-- In order to investigate whether it was necessary to optimize the topological spacing of the HSE element relative to any of the 5 characterized important DNA/protein binding sites